An in silico Approach to Study Bacteria Protein Determinants of Antibiotic Resistance

Parvate, Mohini (School: Dublin Jerome High School)

Antibiotics can be used to cure bacterial infections. Antibiotics target various structures and processes within the cell such as protein synthesis, cell membrane integrity and cell wall synthesis. Antibiotic resistance can occur when vertical or horizontal gene transfer has occurred changing a phenotype of the bacteria. Antibiotic resistant bacteria are not susceptible to antibiotics. Proteins that confer resistance to antibiotics are determined by experimentation and in silico genome analysis. In this project, various bacteria with the same protein determinant were evaluated. The hypothesis is that all bacteria containing a given bacterial protein determinant will be resistant to the antibiotic. To test the hypothesis, the antibiotic tetracycline was selected. Using CARD database resistant protein determinants were acquired. NCBI database was used to obtain the genome sequence of the protein (e.g. TetQ). Then using the BLAST Tool bacteria containing the sequence were searched. Each bacteria was classified as resistant or susceptible using a Antibiotic Resistant Database. It was found that there some bacteria were susceptible in spite of containing the gene that creates the antibiotic resistant protein. The question of why the specific protein fails to confer resistance to the bacteria was evaluated by looking at other proteins generated by those bacteria. This was done by comparing common proteins found in susceptible bacteria. Three antibiotic resistant proteins were analyzed and proteins found only in sensitive bacteria were recorded. It was concluded that these protein have a role in negating the effect of the resistance protein in sensitive bacteria.

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